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S17 System Bioenergetics

17L1

Antioxidant effects induced in biological macromolecular systems by high density photons through localized excitations

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We have recently reported that high density photon fluxes (HDGP), which induce multiphoton processes, generate antioxidant effects in biological systems subjected to ROS (reactive oxygen species) aggression (J.Photochem.Photobiol.B-102, 39–44, 2011). In this paper we present experimental results obtained on protein macromolecules subjected to ultraviolet denaturation. Irradiation with HDGP, in the visible band ($\lambda = 515$ nm), generates localized excitations by polarization effects, with strong antioxidant properties. We studied two specific proteins: superoxide dismutase (SOD), a relevant free radicals "scavenger", and bovine serum albumin (BSA). Under ultraviolet (UV) denaturation, the SOD-enzyme, when simultaneously irradiated with $\lambda = 515$ nm light, preserves its entire activity through a photo isomerization of the Cu–Zn link at the enzymic active center. The UV-irradiation induces a breaking of BSA-molecule as revealed in circular dichroism spectroscopy, with a significant loss of its α-helix content. In our experimental set-up, when BSA is previously irradiated with HDGP, the induced localized excitations reduce the loss of α-helix content from 2.25% to 1.65%. Circular dichroism spectra performed on cellular cultures under UV-irradiation, reveal, when simultaneously irradiated with green light, a protection of the proteins helicticity, through photo isomerization of l–d histidine in the secondary amino acids chain structure. A quantum chemical computation was used to investigate the theoretical basis for these oxidation processes in order to calculate the energetic structure of these molecular states. The calculations were performed using a Gaussian 03W with the Chemisian software. We term biological spectroscopy, this new type of research, in which biological systems are used as detector of subtle physical transitions.

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17L2

Dehydrogenase kinetic parameters determine the electron competition mechanisms in respiratory chain

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In *Saccharomyces cerevisiae*, the most important systems for conveying excess cytosolic NADH to the mitochondrial respiratory chain are the external NADH dehydrogenases (Nde1p and Nde2p) and the glycerol-3-phosphate dehydrogenase shuttle. In the latter system, NADH is oxidized to NAD^+ and dihydroxyacetone phosphate is reduced to glycerol-3-phosphate (G3P) by the cytosolic Gpd1p. G3P donates electrons to the respiratory chain via mitochondrial G3P-dehydrogenase (Gut2p). At saturating concentrations of NADH, the activation of external NADH dehydrogenases completely inhibits glycerol 3-phosphate oxidation. This inhibition is caused by competition for the entrance of electrons into the respiratory chain. Using single deletion mutants of Nde1p or Nde2p, we have shown that glycerol-3-phosphate oxidation via Gut2p is inhibited fully when NADH is oxidized via Nde1p, whereas only 50% of glycerol-3-phosphate oxidation is inhibited when Nde2p is functioning. Moreover, we show that electrons from Nde1p are favored over electrons coming from Ndip (internal NADH dehydrogenase) and that when electrons come from either Nde1p or Nde2p and succinodehydrogenase, their use by the respiratory chain is shared to a comparable extent [1]. This suggests a specific competition for electron entrance into the respiratory chain, which is not due to the supramolecular organization of the respiratory chain [2]. Such a competition generates a priority for cytosolic NADH reoxidation. By determining the kinetic parameters of different external dehydrogenases and using a stochastic model derived for the complex I, we showed that the different processes of electron competition observed in various yeast strains may be due to the particular kinetic parameters of the involved dehydrogenases.

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17L3

Conversion of *Corynebacterium glutamicum* from an aerobic respiring to an aerobic fermenting bacterium by inactivation of the respiratory chain

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